

[illegible]

(Nucleotide) FASTA of: con-mc4r.seq from: 1 to: 746 April 10, 1998 19:52

Searching with both strands of the query.
Scoring matrix: GenRunData:fastadna.cmp
Constant pamfactor used
Gap creation penalty: 16 Gap extension penalty: 4

```
con-mc4r.seq
/usr2/users/rothschi/kwan/mc4r/seq/s77415.gb_pr

LOCUS          S77415          1671 bp      DNA          PRI          26-SEP-1995
DEFINITION     melanocortin-4 receptor [human, Genomic, 1671 nt].
ACCESSION      S77415
NID            g998456
KEYWORDS       .
SOURCE         human. . . .
```

(SEA ID No:3)
con-mc4r.seq

10 20 30
ACAAGAACTCTGCATTCCACCATGTACTTTT

```

s77415      ATATCTTAGTGATTGTGGCAATAGCCAAGAACAAGATCTGCATTACCCATGTACTTTT
(500 ID NO:2) 580          590          600          610          620          630

              40          50          60          70          80          90
con-mc4r.seq TCATCTGTAGCCTGGCTGTGGCTGATATGCTGGTGAGCGTTTCCAATGGGTCAGAAACCA
|||||
s77415      TCATCTGCAGCTTGGCTGTGGCTGATATGCTGGTGAGCGTTTCAATGGATCAGAAACCA
640          650          660          670          680          690

              100         110         120         130         140         150
con-mc4r.seq TTGTCATCACCCCTATTAAACAGCACGGACACGGACGCACAGAGTTTCACAGTGAATATTG
|||||
s77415      TTATCATCACCCCTATTAAACAGTACAGATACGGATGCACAGAGTTTCACAGTGAATATTG
700          710          720          730          740          750

```

con-mc4r.seq ATAATGTCATTGACTCAGTGATCTGTAGCTCCTTACTCGCCTCAATTTGCAGCCTGCTTT
|||||
s77415 ATAATGTCATTGACTCGGTGATCTGTAGCTCCTTGTGATCCATTTGCAGCCTGCTTT
760 770 780 790 800 810

con-mc4r.seq CGATTGCAGTGGACAGGTATTTTACTATCTTTTATGCTCTCCAGTACCATAACATTATGA
|||||
s77415 CAATTGCAGTGGACAGGTACTTTTACTATCTTTCTAIGCTCTCCAGTACCATAACATTATGA
820 830 840 850 860 870

con-mc4r.seq CAGTTAAGCGGGTTGGAATCATCATCAGTTGTATCTGGGCAGTCTGCACGGTGTGGGGTG
|||||
s77415 CAGTTAAGCGGGTTGGGATCAGCATAGTTGTATCTGGGCAGTCTGCACGGTTTCAGGCA
880 890 900 910 920 930

con-mc4r.seq TTTTGTTCATCATTTTACTCAGATAGCAGTGCTGTTATTATCTGCCTCATACCGTGTCT
|||||
s77415 TTTTGTTCATCATTTTACTCAGATAGTAGTGCTGTATCATCTGCCTCATCACCATGTCT
940 950 960 970 980 990

con-mc4r.seq TCACCATGCTGGCTCTCATGGCTTCTCTATGTCCACATGTTCTCATGGCCAGACTCC
|||||
s77415 TCACCATGCTGGCTCTCATGGCTTCTCTATGTCCACATGTTCTGATGGCCAGGCTTC
1000 1010 1020 1030 1040 1050

con-mc4r.seq ACATTAAGAGGATCGCCGCTCTCCAGGCACTGGCACCATCCGCCAAGGTGCCAACATGA
|||||
s77415 ACATTAAGAGGATGCTGTCTCTCCCGGCACTGGTGCCATCCGCCAAGGTGCCAATATGA
1060 1070 1080 1090 1100 1110

con-mc4r.seq AGGGGGCAATTACCCTGACCATCTTGATTGGGGTCTTTGTGGTCTGCTGGGGCCCCCTTCT
|||||
s77415 AGGGGAGCGATTACCTTGACCATCTTGATTGGGCTCTTTGTGTCTGCTGGGGCCCCATCT
1120 1130 1140 1150 1160 1170

con-mc4r.seq TCCTCCACTTAATATTCTATATCTCTGCCCCAGAAATCCATACTGTGTGTGCTTCATGT
|||||
s77415 TCCTCCACTTAATATTCTATATCTCTGCTCCAGAAATCCATATTGTGTGTGCTTCATGT
1180 1190 1200 1210 1220 1230

con-mc4r.seq CTCACTTTAATTTGTATCTCATCCTGATCATGTGTAATTCATCATCAATCCCCTGATT
|||||
s77415 CTCACTTTAATTTGTATCTCATCCTGATCATGTGTAATTCATCATCAATCCCCTGATT
1240 1250 1260 1270 1280 1290

con-mc4r.seq ATGCACTCCGGAGCCAAGAACTGAGGAAAACCTTCAAGAGATCATCTGTTGCTAT
|||||
s77415 ATGCACTCCGGAGTCAAGAACTGAGGAAAACCTTCAAGAGATCATCTGTTGCTATCCCC
1300 1310 1320 1330 1340 1350

s77415 TGGGAGGCCTTTGTGACTTGTCTAGCAGATATTAAATGGGGACAGAGCACGCAATATAGG
1360 1370 1380 1390 1400 1410

(Peptide) TFASTA of: human.pep from: 1 to: 332 April 9, 1998 16:18

TO: mc4r-alle*.seq Sequences: 2 Symbols: 1,492 Word Size: 2

Scoring matrix: GenRunData:blosun50.cmp

Variable pamfactor used

Gap creation penalty: 16 Gap extension penalty: 4

The best scores are: frame initl initn opt..

```

/usr2/users/rothschi/kwan/mc4r/seq/mc4r-allele1.seq      Begin: 3      End: 746
! mc4r-allele1.seq Length: 746 April ... (3) 1602 1602 1602
/usr2/users/rothschi/kwan/mc4r/seq/mc4r-allele2.seq      Begin: 3      End: 746
! mc4r-allele2.seq Length: 746 April ... (3) 1596 1596 1596

```

SCORES Frame: (3) Init1: 1602 Initn: 1602 Opt: 1602
97.6% identity in 248 aa overlap

```

(SEQ ID NO:4)
human.pep      50      60      70      80      90      100
QLFVSPEVFVTLGVISLLENILVIVAIAKKNLHSPMYFFICSLAVADMLVSVSNGSETI
|||||
KNLHSPMYFFICSLAVADMLVSVSNGSETI
10      20      30

mc4r-allele
(SEQ ID NO:5)

110      120      130      140      150      160
human.pep      IITLLNSTDTDAQSFVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT
:|||||
mc4r-allele      VITLLNSTDTDAQSFVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT
40      50      60      70      80      90

170      180      190      200      210      220
human.pep      VKRVGISISCIWAAC TVSGILFIIYSDSSAVIICLITMFFTMLALMASLYVHMFIMARLH
||||| :||||| :||||| :||||| :|||||
mc4r-allele      VKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFIMARLH
100      110      120      130      140      150

230      240      250      260      270      280
human.pep      IKRIAVLPGTGAI RQGANKGAITLTILIGVFVCWAPFFLHLIFYISCPQNPYCVCFMS
||||| :||||| :||||| :||||| :|||||
mc4r-allele      IKRIAVLPGTG TIRQGANKGAITLTILIGVFVCWAPFFLHLIFYISCPQNPYCVCFMS
160      170      180      190      200      210

290      300      310      320      330
human.pep      HFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICCYPLGGLCDLSSRY
|||||
mc4r-allele      HFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICCY
220      230      240

```

human.pep
/usr2/users/rothschi/kwan/mc4r/seq/mc4r-allele2.seq

SCORES Frame: (3) Init1: 1596 Initn: 1596 Opt: 1596
97.2% identity in 248 aa overlap

	50	60	70	80	90	100
human.pep	QLFVSPEVFVTLGVISLLENILVIVAIKKNLHSPMYFFICSLAVADMLVSVSNGSETI					
mc4r-allele2	KNLHSPMYFFICSLAVADMLVSVSNGSETI					
	10	20	30			
	110	120	130	140	150	160
human.pep	IITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT					
	:					
mc4r-allele2	VITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT					
	40	50	60	70	80	90
	170	180	190	200	210	220
human.pep	VKRVGISISCIWAAC TVSGILFIIYSDSSAVIICLITMFFTMLALMASLYVHMFMLMARLH					
	:					
mc4r-allele2	VKRVGIIISCIWAVCTVSGVLFIIYSDSSAVIICLITVFFTMLALMASLYVHMFMLMARLH					
	100	110	120	130	140	150
	230	240	250	260	270	280
human.pep	IKRIAVLPGTGAIROGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMS					
	:					
mc4r-allele2	IKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMS					
	160	170	180	190	200	210
	290	300	310	320	330	
human.pep	HFNLYLILIMCNSIIDPLIYALRSQELRKTFKEIICCYPLGGLCBLSSRY					
mc4r-allele2	HFNLYLILIMCNSIINPLIYALRSQELRKTFKEIICCY					
	220	230	240			

! CPU time used:

! Database scan: 0:00:00.2

! Post-scan processing: 0:00:00.1

! Total CPU time: 0:00:00.4

! Output File: human.tfasta

001220 67103660

LINKAGE REPORT OF TWO-POINT ANALYSIS

New locus MC4R

in sex-equal linkage analyses with existing loci

S0082	MC4R	rec. frags.=	0.05,	lods =	14.74
CGA	MC4R	rec. frags.=	0.14,	lods =	6.88
S0020	MC4R	rec. frags.=	0.18,	lods =	5.32
S0079	MC4R	rec. frags.=	0.12,	lods =	10.35
S0155	MC4R	rec. frags.=	0.14,	lods =	7.68
S0122	MC4R	rec. frags.=	0.18,	lods =	5.17
S0313	MC4R	rec. frags.=	0.00,	lods =	17.76
S0312	MC4R	rec. frags.=	0.20,	lods =	5.60
S0311	MC4R	rec. frags.=	0.17,	lods =	7.18
S0416	MC4R	rec. frags.=	0.20,	lods =	3.21
S0331	MC4R	rec. frags.=	0.02,	lods =	21.91
S0396	MC4R	rec. frags.=	0.16,	lods =	7.85
BHT0433	MC4R	rec. frags.=	0.02,	lods =	21.32
S0536	MC4R	rec. frags.=	0.03,	lods =	15.61
CAPN3	MC4R	rec. frags.=	0.12,	lods =	6.65
KGF	MC4R	rec. frags.=	0.09,	lods =	6.46
MEF2A	MC4R	rec. frags.=	0.05,	lods =	14.36
MC4R	MC4R	rec. frags.=	0.00,	lods =	26.19

in sex-specific (female/male) linkage analyses with existing loci

S0082	MC4R	rec. fracs.=	0.00	0.09,	lods =	15.86
CGA	MC4R	rec. fracs.=	0.07	0.22,	lods =	7.46
S0020	MC4R	rec. fracs.=	0.00	0.25,	lods =	6.33
S0079	MC4R	rec. fracs.=	0.00	0.19,	lods =	11.48
S0155	MC4R	rec. fracs.=	0.00	0.24,	lods =	9.98
S0122	MC4R	rec. fracs.=	0.00	0.27,	lods =	7.10
S0313	MC4R	rec. fracs.=	0.00	0.00,	lods =	17.76
S0312	MC4R	rec. fracs.=	0.04	0.29,	lods =	7.45
S0311	MC4R	rec. fracs.=	0.00	0.28,	lods =	9.02
S0416	MC4R	rec. fracs.=	0.00	0.31,	lods =	4.17
S0331	MC4R	rec. fracs.=	0.05	0.00,	lods =	22.14
S0396	MC4R	rec. fracs.=	0.03	0.24,	lods =	9.33
BHT0385	MC4R	rec. fracs.=	0.14	0.36,	lods =	3.46
BHT0433	MC4R	rec. fracs.=	0.05	0.00,	lods =	21.82
S0536	MC4R	rec. fracs.=	0.00	0.05,	lods =	15.77
CAPN3	MC4R	rec. fracs.=	0.00	0.18,	lods =	7.35
KGF	MC4R	rec. fracs.=	0.00	0.17,	lods =	6.74
MEF2A	MC4R	rec. fracs.=	0.10	0.00,	lods =	14.52
MC4R	MC4R	rec. fracs.=	0.00	0.00,	lods =	26.19

0	ESR	0.18	18.4	0.0
1	S0008	0.12	11.9	18.4
7	CGA	0.03	2.8	30.3
3	S0312	0.05	4.9	33.1
4	S0122	0.09	9.4	38.1
8	KGF	0.06	5.8	47.4
6	CAPN3	0.02	2.5	53.2
9	MEF2A	0.06	6.1	55.7
5	MC4R	0.06	5.6	61.8
10	S0313	0.00	0.0	67.4
11	S0082	0.03	3.4	67.4
12	S0079	0.03	2.5	70.8
14	S0142	0.01	1.0	73.3
13	S0020	0.04	4.3	74.4
15	S0311	0.00	0.0	78.7
16	S0155	0.12	12.2	78.7
17	S0113	0.20	21.0	90.9
18	S0302	0.22	23.4	111.9
19	S0112			135.3

* denotes recomb. frac. held fixed in this analysis. log10_like = -305.098

FIGURE 5.

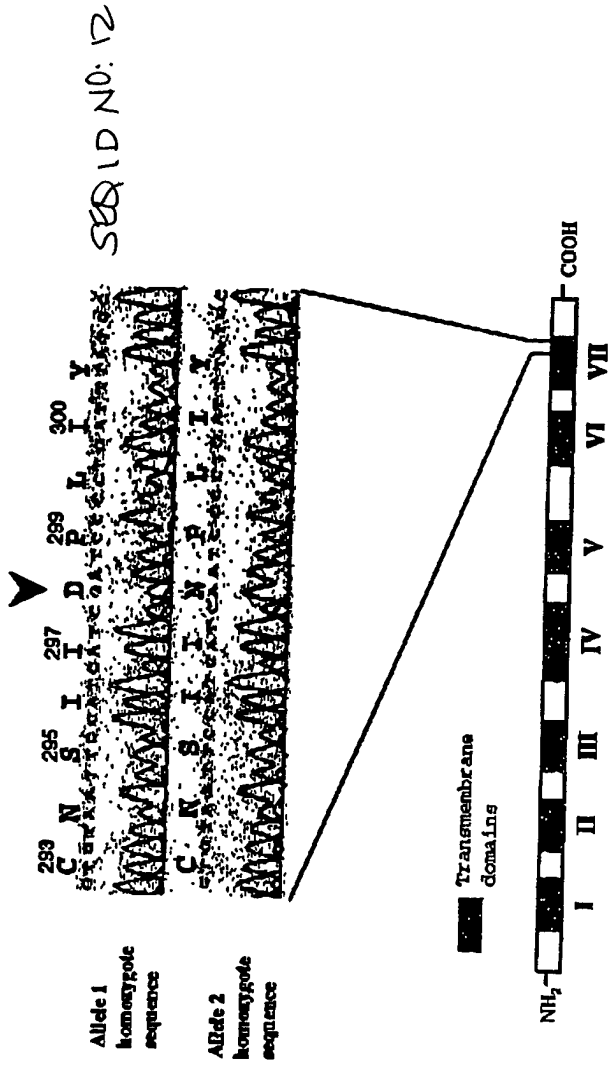


FIGURE 6.



FIGURE 7.

